

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 11

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

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(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 31-Mar-1997

(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1007R1

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids
(B) TYPE: Amino Acid
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 20 25 30
Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
25 35 40 45
Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60
Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
65 70 75
Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
30 80 85 90
Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
95 100 105
35 Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly

110

115

120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro

125

130

135

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Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His

140

145

150

Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys

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155

160

165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro

170

175

180

15

Thr

181

(2) INFORMATION FOR SEQ ID NO:2:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50

30

TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150

35

ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200

TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250

TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300

5 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350

CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20

CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CAGGGCCCCG CAGTCTAGGC ATGATTGG 28

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1438 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCC GCCTCC 250
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
AGATTGGTCT GTTTTGTTCG AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600

AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCT 650

GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700

5 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750

CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800

TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850

10 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900

CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950

15 GGCGGCTGGG AGCAGAGCAG GGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000

CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050

GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100

20 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150

CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200

25 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250

CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300

ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350

30 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400

TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15

10

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 25 30

15

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60

20

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
80 85 90

25

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
110 115 120

30

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
125 130 135

35

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His

		140		145		150
	Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys					
		155		160		165
5	Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro					
		170		175		180
	Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys					
10		185		190		195
	Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu					
		200		205		210
15	Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg					
		215		220		225
	His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly					
		230		235		240
20	Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu					
		245		250		255
	Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys					
25		260		265		270
	Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr					
		275		280		285
30	Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp					
		290		295		300
	Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr					
		305		310		315
35						

Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln
320 325 330

Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg
335 340 345

Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu
350 355 360

Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln
365 370 375

Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu
380 385 390

Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94

Met Glu

1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133

Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu

5

10

15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr

20

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CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
 30 35 40

5 AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
 45 50

10 CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
 55 60 65

15 TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 70 75 80

TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
 85 90

20 GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406
 Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn
 95 100 105

25 TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445
 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro
 110 115

30 GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484
 Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser
 120 125 130

35 AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523
 Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly
 135 140 145

GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562
 Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg
 150 155

5 GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601
 Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu
 160 165 170

10 CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640
 His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu
 175 180

15 GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679
 Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp
 185 190 195

AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718
 Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu
 200 205 210

20 GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757
 Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr
 215 220

25 TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796
 Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala
 225 230 235

30 GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835
 Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala
 240 245

35 ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874
 Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu
 250 255 260

GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913
 Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln
 265 270 275

5 TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952
 Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
 280 285

10 CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991
 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp
 290 295 300

15 CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030
 Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro
 305 310

20 ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069
 Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
 315 320 325

25 ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108
 Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp
 330 335 340

30 GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147
 Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr
 345 350

35 CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186
 Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val
 355 360 365

40 GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225
 Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu
 370 375

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
380 385 390

5 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

10 GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

15 CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490

20 CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

15